The human homolog of ribosomal protein S18

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In order to identify new genes preferentially expressed in cytotrophoblasts of first trimester placenta, which display phenotypical characteristics similar to tumor cells, we have made a subtracted cDNA library. The library represents early placental, cytotrophoblastic, endoplasmic reticular membrane-bound RNA in the 0.5—2 kb size range, from which common sequences with terminal placenta and EL-2 activated T lymphocytes have been removed. Recombinant cDNA were analyzed by differential screening. Clones displaying a preferential expression in early placenta after Southern blot analysis were selected and sequenced.

We have thus focused our study on five clones, the level of expression of which was analyzed by Northern blot in various tissues. One of these, designated B9, was expressed sparsely in terminal placenta and with varying levels in most other tissues. Detailed sequence analysis was performed, revealing 549 bp containing a polyadenylation signal and an open reading frame of 152 amino acids. This ORF starts with an ATG codon, which occurs in the context CAGCCATGT, differing in 3 positions from the optimal sequence CCACCATGC (1). TAA is used as stop codon.

Database search using the FASTA program (2), showed 90.7% nucleic acid and 100% amino acid homology with the mouse KE3 sequence as shown below. The corresponding rat amino acid sequence as predicted from cDNA was also described to be 100% identical (3). The predicted KE3 gene product, which remains putative until in vivo proof is obtained, has been described as the ribosomal protein S18 based on homology with bacterial ribosomal protein S13 and the electrophoretic properties of the in vitro translation product (4). The sequence also shows a structural homology with fos-related molecules based on the heptad repeat of leucine residues (leucine zipper) preceded by a basic region shown below as asterisks (5). PROSITE (A.Bairoch) analysis reveals six putative phosphorylation sites.

The KE3 gene belongs to a group of six genes (KE1-5 and SET), located in the H-2K region of the murine MHC (6). A homolog of this region has also been localized in the human major histocompatibility complex (7).

REFERENCES

Figure 1.